IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Appl. No.	:	10/613,053	Confirmation No.: 6718
Applicant	:	Jun Imamura	
Filed	:	July 7, 2003	
Group Art Unit	:	1638	
Examiner	:	FOX, David T.	
For	:	Protein Involved in Restoration of Cytoplasmic Male Sterility to Fertility and Gene Encoding the Protein and Gene	
Docket No.	:	54-05A	
Customer No.	:	23713	

Declaration under 37 CFR 1.132

I, James Coburn, declare that:

1. I am the President and CEO of Harbor Consulting IP Services, Inc. of Portsmouth, New Hampshire, a company in the business of sequence listing preparation, sequence searching and sequence alignment comparison projects. Harbor Consulting IP Services, Inc. has been in operation since the fall of 1995. All technical staff of Harbor Consulting IP Services, Inc. have science degrees in biological fields such as biochemistry, molecular biology, and biology, and are familiar with nucleic acid and amino acid sequences and sequence comparisons.

2. On October 3, 2008, we received a series of nucleic acid and amino acid sequences from Michael Curtis of Greenlee, Winner and Sullivan, P.C. for the purpose of comparing the relative sequence homology of the provided sequences. Each sequence was provided and identified by Michael Curtis.

3. In particular, we were asked to compare the sequences as follows:

Group 1 - the 54-05A application (10/613,053) compared with Brown Patent No. 1 (7,071,375)

- DNA sequences designated as SEQ 1 and SEQ 2 from the 54-05A application (10/613,053) compared with sequences designated as SEQ 32 and SEQ 87 (nucleotides 103,375-105,589) from Brown Patent No. 1 (7,071,375).

- Amino acid sequence designated as SEQ 3 from the 54-05A application with amino acid sequence designated as SEQ 31 from Brown Patent No. 1.

Group 2 - the 54-05A application (10/613,053) compared with Brown Patent No. 2 (7,314,971)

- DNA sequences designated as SEQ 1 and SEQ 2 from the 54-05A application (10/613,053) with sequences designated as SEQ 87 (nucleotides 164,311-174,022; nucleotides 167,079-173,669; and nucleotides 167,079-173,669 with the intron at nucleotides 167,459-167,585 removed) from Brown Patent No. 2 (7,314,971).
- Amino acid sequence designated as SEQ 3 from the 54-05A application with amino acid sequence designated as SEQ 179 from Brown Patent No. 2.

Group 3 - the 54-05A application (10/613,053) compared with the Japanese applications from April 2001 (JP 2001-128008), July 2001 (JP 2001-202082) and January 2002 (JP 2002-020083)

- DNA sequence designated as SEQ 1 from the 54-05A application (10/613,053) with sequences designates as SEQ 1 from each of the three Japanese applications (JP 2001-128008, JP 2001-202082 and JP 2002-020083).
- Sequence designated as SEQ 2 from the 54-05A application with DNA sequences designated as SEQ 2 from each of the three Japanese applications (JP 2001-128008, JP 2001-202082 and JP 2002-020083).
- Amino acid designated as SEQ 3 from the 54-05A application with sequences designated as SEQ 3 from each of the three Japanese applications.

Group 4 - the 54-05A application (10/613,053) compared with the Brown provisional applications (60/305,026; 60/305,363 and 60/308,736)

- Sequence designated as SEQ 1 from the 54-05A application (10/613,053) with sequences designated as the large genomic sequence from both Brown Provisional No. 1 (60/305,026) and Brown Provisional No. 3 (60/308,736).
- Sequence designated as SEQ 2 from the 54-05A application with each DNA sequence in each of the three Brown provisional applications (60/305,026; 60/305,363 and 60/308,736).
- Amino acid sequence designated as SEQ 3 from the 54-05A application with each amino acid sequence in each of the three Brown provisional applications (60/305,026; 60/305,363 and 60/308,736).

Group 5 - the Japanese applications from April 2001 (JP 2001-128008) and January 2002 (JP 2002-020083) compared with the Brown provisional applications (60/305,026; 60/305,363 and 60/308,736)

- Amino acid sequence designated as SEQ 3 from the Japanese applications from April 2001 (JP 2001-128008) and January 2002 (JP 2002-020083) with each amino acid sequence in each of the three Brown provisional applications (60/305,026; 60/305,363 and 60/308,736).

4. Between October 3rd - October 9th, 2008, the above sequences were aligned and compared using the BLAST algorithm, which is a standard and well known method in the industry for aligning two nucleic acid sequences or two amino acid sequences and determining the level of sequence homology/identify between two sequences. In bioinformatics, **B**asic **L**ocal **A**lignment **S**earch **T**ool, or **BLAST**, is an algorithm for comparing primary biological sequence information, such as the amino-acid sequences of different proteins or the nucleotides of DNA sequences. The BLAST program was designed by Eugene Myers, Stephen Altschul, Warren Gish, David J. Lipman and Webb Miller at the NIH and was published in J. Mol. Biol. in 1990.

5. The results of the sequence comparisons are provided in Sequence Reports 1-5 attached hereto which correspond to the comparison groups 1-5 listed above. The results are presented in terms of percentage of sequence homology as recognized in the industry.

6. In several sequence comparisons, our reports indicate that "No significant similarity was found." In these instances, the compared sequences were so dissimilar that no meaningful alignment of the sequences could be obtained. In other words, it is not possible in these cases to report any level of sequence homology.

7. I further declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and

further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code, and that such willful false statements may jeopardize the validity of the above-referenced application or any patent issuing thereon.

Oct. 15, 2008
Date

James Coburn

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